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IIA1 V_H (SEQ ID NO: 1):

QVQLKESGPGLVAPSQSLISITCTISGFSLTDYGVHWVRQPPGKGLEWLVVIWSDGSSTYNALKSRMTI
RKDNSKSQVFLIMNSLQTDDSAMYYCARHGTYYGMTTGALDYWGQGTSVTVSS

V_H 1.0 (SEQ ID NO: 2):

QVQLVESGGGLVQPQGGSLRISCAISGFSLTDYGVHWVRQAPGKGLEWLVVIWSDGSSTYNALKSRMT
ISKDNSKSTVYLQMNSLRAEDTAMYYCARHGTYYGMTTGALDYWGQGTLTVSS

V_H 2.0 (SEQ ID NO: 3):

EVQLVESGGGLVQPQGGSLRISCAISGFSLTDYGVHWVRQAPGKGLEWLVVIWSDGSSTYNALKSRMT
ISKDNSKNTVYLQMNSLRAEDTAVYYCARHGTYYGMTTGALDYWGQGTLTVSS

V_H 3.0 (SEQ ID NO: 4):

EVQLVESGGGLVQPQGGSLRISCAISGFSLTDYGVHWVRQAPGKGLEWLVVIWSDGSSTYNALKSRF
TISRDN SKNTLYLQMNSLRAEDTAVYYCARHGTYYGMTTGALDYWGQGTLTVSS

V_H 4.0 (SEQ ID NO: 5):

EVQLVESGGGLVQPQGGSLRISCAISGFSLTDYGVHWVRQAPGKGLEWLVVIWSDGSSTYNALKSRM
TISKDNSKSTVYLQMNSLRAEDTAVYYCARHGTYYGMTTGALDYWGQGTLTVSS

V_H 5.0 (SEQ ID NO: 6):

QVQLVESGGGLVQPQGGSLRISCAISGFSLTDYGVHWVRQAPGKGLEWLVVIWSDGSSTYNALKSRMT
ISKDNSKSTVYLQMNSLRAEDTAMYYCARHGTYYGMTTGALDYWGQGTLTVSS

IIA1 V_L (SEQ ID NO: 7):

QIVLTQSPAIMSASLGERVMTCTASSSVSSNYLHWYQQKPGSAPNLWIYSTSNLASGVPARFSGSGSG
TSYSLTISSMEAEDAATYYCHQYLRSPPTFGGGTKLEIKR

V_L 1.0 (SEQ ID NO: 8):

DIQLTQSPSSMSASLGDRVMTCTASSSVSSNYLHWYQQKPGKAPNLWIYSTSNLASGVPSRFSGSGSG
TDYTLTISSMQPEDFATYYCHQYLRSPPTFGQGTTKLEIKR

V_L 2.0 (SEQ ID NO: 9):

DIQLTQSPSSLSASVGDRVMTCTASSSVSSNYLHWYQQKPGKAPKLWIYSTSNLASGVPSRFSGSGSG
TDYTLTISSMQPEDFATYYCHQYLRSPPTFGQGTTKLEIKR

V_L 3.0 (SEQ ID NO: 10):

DIQMTQSPSSLSASVGDRVITCTASSSVSSNYLHWYQQKPGKAPKLLIYSTSNLASGVPSRFSGSGSGT
DFTLTISLQPEDFATYYCHQYLRSPPTFGQGTTKVEIKR

V_L 4.0 (SEQ ID NO: 11):

DIQLTQSPSSLSASVGDRVMTCTASSSVSSNYLHWYQQKPGKAPKLWIYSTSNLASGVPSRFSGSGSGT
DYTLTISSLQPEDFATYYCHQYLRSPPTFGQGTTKVEIKR

V_L 5.0 (SEQ ID NO: 12):

DIQLTQSPSSLSASVGDRVMTCTASSSVSSNYLHWYQQKPGKAPKLWIYSTSNLASGVPSRFSGSGSG
TDYTLTISSLQPEDFATYYCHQYLRSPPTFGQGTTKVEIKR

FIGURE 1

	<u>V_L</u>	<u>FR₁</u>	<u>CDR₁</u>	<u>FR₂</u>	<u>CDR₂</u>	<u>FR₃</u>	<u>CDR₃</u>	<u>FR₄</u>
I1A1	V _H	QVQLKESGPGLIVAPSQSLISITCTIS	GFSLTDYGVH	WYRQAPGKGLEWLW	VIWSDGSSTNSALKS	RMTIRKDNSKSQVFLIMNSLOTDDSAMYYCAR	HGTYYGMTTTGDA LDY	WGQGTTSVTVSS
	V _H 1.0	QVOLVESGPGLIVQPGGSLRISCAIS	GFSLTDYGVH	WYRQAPGKGLEWLW	VIWSDGSSTNSALKS	RMTISKDN SKTSTVYLQNSLRAEDT AMYYCAR	HGTYYGMTTTGDA LDY	WGQGTTSVTVSS
	V _H 2.0	EVQLVESGGSLIVQPGGSLRISCAIS	GFSLTDYGVH	WYRQAPGKGLEWLW	VIWSDGSSTNSALKS	RMTISKDN SKTSTVYLQNSLRAEDT AMYYCAR	HGTYYGMTTTGDA LDY	WGQGTTSVTVSS
	V _H 3.0	EVQLVESGGSLIVQPGGSLRISCAIS	GFSLTDYGVH	WYRQAPGKGLEWLW	VIWSDGSSTNSALKS	RFTISRDNSKNTLYLQNSLRAEDT AMYYCAR	HGTYYGMTTTGDA LDY	WGQGTTSVTVSS
	V _H 4.0	EVQLVESGGSLIVQPGGSLRISCAIS	GFSLTDYGVH	WYRQAPGKGLEWLW	VIWSDGSSTNSALKS	RMTISKDN SKTSTVYLQNSLRAEDT AMYYCAR	HGTYYGMTTTGDA LDY	WGQGTTSVTVSS
	V _H 5.0	QVQLVESGGSLIVQPGGSLRISCAIS	GFSLTDYGVH	WYRQAPGKGLEWLW	VIWSDGSSTNSALKS	RMTISKDN SKTSTVYLQNSLRAEDT AMYYCAR	HGTYYGMTTTGDA LDY	WGQGTTSVTVSS
I1A1	V _L	QIVLTQSPAIMSASLGERVTMTC	TASSSVSSNYLH	WYQQKPGPSAPNLWY	STSNLAS	GYPARFSGSGSGTYSU LTISSMMAEDAATYC	HQYLRSPP	FGGGTKEI KR
	V _L 1.0	DIGLTQSSMSASLGDRVTMTC	TASSSVSSNYLH	WYQQKPGKAPNLWY	STSNLAS	GYPSRFSGSGSGTIDT LTISSMOPEDFATYC	HQYLRSPP	FGQGTKEI KR
	V _L 2.0	DIGLTQSSLSASVCDRTMTC	TASSSVSSNYLH	WYQQKPGKAPKLWY	STSNLAS	GYPSRFSGSGSGTIDT LTISSMOPEDFATYC	HQYLRSPP	FGQGTKEI KR
	V _L 3.0	DIQMTQSPSSLSASVCDRTVTC	TASSSVSSNYLH	WYQQKPGKAPKLWY	STSNLAS	GYPSRFSGSGSGTIDT LTISSMOPEDFATYC	HQYLRSPP	FGQGTKEI KR
	V _L 4.0	DIQLTQSPSSLSASVCDRTVTC	TASSSVSSNYLH	WYQQKPGKAPKLWY	STSNLAS	GYPSRFSGSGSGTIDT LTISSMOPEDFATYC	HQYLRSPP	FGQGTKEI KR
	V _L 5.0	DIQLTQSPSSLSASVCDRTMTC	TASSSVSSNYLH	WYQQKPGKAPKLWY	STSNLAS	GYPSRFSGSGSGTIDT LTISSMOPEDFATYC	HQYLRSPP	FGQGTKEI KR

FIGURE 2

A. IIA1 V_H sequences

[NA, SEQ ID NO: 13; AA, SEQ ID NO: 1]

1 ATGGCTGTCCTGGGGCTGCTTCTGCCTGGTGACTTCCCAAGCTGTGCCTGTCCCAG
M A V L G L L L C L V T F P S C V L S Q
61 GTGCAGCTGAAGGAGTCAGGACCTGGCCTGGCGCCCTCACAGAGCCTGTCATCACA
V Q L K E S G P G L V A P S Q S L S I T
121 TGCACCACATCTCAGGGTTCTCATTAACCGACTATGGTGTCACTGGGTTGCCAGCCTCCA
C T I S G F S L T D Y G V H W V R Q P P
181 GGAAAGGGTCTGGAGTGGCTGGTAGTGATTTGGAGTGATGGAAGCTCAACCTATAATTCA
G K G L E W L V V I W S D G S S T Y N S
241 GCTCTCAAATCCAGAACATGACCATCAGGAAGGACAACCTCCAAGAGCCAAGTTCTTAATA
A L K S R M T I R K D N S K S Q V F L I
301 ATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGTGCCAGACATGGAACCTAC
M N S L Q T D D S A M Y Y C A R H G T Y
361 TACGGTATGACTACGACGGGGATGCTTGGACTACTGGGTCAAGGAACCTCAGTCACC
Y G M T T T G D A L D Y W G Q G T S V T
421 GTCTCCTCA
V S S

B. IIA1 V_L sequences

[NA, SEQ ID NO: 14; AA, SEQ ID NO: 7]

1 ATGGATTTCAGGTGCAGATTTCAGCTTCTGCTAATCAGTGCCTCAGTCATAATGTCC
M D F Q V Q I F S F L L I S A S V I M S
61 AGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCTAGGGAACGG
R G Q I V L T Q S P A I M S A S L G E R
121 GTCACCATGACCTGCACTGCCAGTTCAAGTGTAAAGTCCAATTACTTGCCTGGTACCAAG
V T M T C T A S S S V S S N Y L H W Y Q
181 CAGAAGCCAGGATCCGCCCAATCTCTGGATTATAGCACATCCAACCTGGCTTCTGG
Q K P G S A P N L W I Y S T S N L A S G
241 GTCCCAGCTCGTTCAAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAAATCAGCAGC
V P A R F S G S G S G T S Y S L T I S S
301 ATGGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCTCGTCCCCACCGACG
M E A E D A A T Y Y C H Q Y L R S P P T
361 TTCGGTGGAGGCACCAAGCTGGAAATCAAA
F G G G T K L E I K

FIGURE 3

A. Antibody 200-4 V_H sequences
[NA, SEQ ID NO: 15; AA, SEQ ID NO: 16]

```

1   ATGGCTGTCCCTGGGGCTGCTTCTCGCCTGGTGACTTCCCAGCTGTGCCTGTCCCAG
      M A V L G L L C L V T F P S C V L S Q
61   GTGCAGCTGAAGGAGTCAGGACCTGGCCTGGCGCCCTCACAGAGCCTGTCCATCACA
      V Q L K E S G P G L V A P S Q S L S I T
121  TGCACCATCTCAGGGTTCTCATTAACCGACTATGGTGTCACTGGGTTGCCAGCCTCCA
      C T I S G F S L T D Y G V H W V R Q P P
181  GGAAAGGGTCTGGAGTGGCTGGTAGTGATTTGGAGTGATGGAAGCTCAACCTATAATTCA
      G K G L E W L V V I W S D G S S T Y N S
241  GCTCTCAAATCCAGAATGACCATCAGGAAGGACAACCTCCAAGAGCCAAGTTTCTTAATA
      A L K S R M T I R K D N S K S Q V F L I
301  ATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGTGCCAGACATGGAACATTAC
      M N S L Q T D D S A M Y Y C A R H G T Y
361  TACGGTATGACTACGACGGGGATGCTTGGACTACTGGGGTCAAGGAACCTCAGTCACC
      Y G M T T T G D A L D Y W G Q G T S V T
421  GTCTCGAGC
      V S S

```

B. Antibody 200-4 V_L sequences
[NA, SEQ ID NO: 17; AA, SEQ ID NO: 18]

```

1   ATGGATTTCAAGGTGCAGATTTCACTCAGCTTCTGCTAACAGTCAGTCATAATGTCC
      M D F Q V Q I F S F L L I S A S V I M S
61   AGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCATCTCTAGGGAACGG
      R G Q I V L T Q S P A I M S A S L G E R
121  GTCACCATGACCTGCACTGCCAGTTCAAGTGTAAAGTCCAATTACTTGCACGGTACCCAG
      V T M T C T A S S S V S S N Y L H W Y Q
181  CAGAACCCAGGATCCGCCCAATCTCTGGATTATAGCACATCCAACCTGGCTTCTGGA
      Q K P G S A P N L W I Y S T S N L A S G
241  GTCCCAGCTCGTTCACTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGC
      V P A R F S G S G S G T S Y S L T I S S
301  ATGGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCTCGTCCCCACCGACG
      M E A E D A A T Y Y C H Q Y L R S P P T
361  TTCGGTGGAGGCACCAAGCTCGAGATCAA
      F G G G T K L E I K

```

FIGURE 4

A. M200 V_H sequences
[NA, SEQ ID NO: 19; AA, SEQ ID NO: 20]

```

1   TCTAGACCACCATGGCTGTCCTGGGGCTGCTTCTCTGCCTGGTACTTCCCAAGCTGTG
      M A V L G L L C L V T F P S C
61   TCCTGTCCCAGGTGCAGCTGAAGGAGTCAGGACCTGGCTGGTGGCGCCCTCACAGAGCC
      V L S Q V Q L K E S G P G L V A P S Q S
121  TGTCCCATCACATGCACCATCTCAGGGTTCTCATTAACCGACTATGGTGTTCACTGGGTC
      L S I T C T I S G F S L T D Y G V H W V
181  GCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGTAGTGATTGGAGTGATGGAAGCTCAA
      R Q P P G K G L E W L V V I W S D G S S
241  CCTATAATTCAGCTCTCAAATCCAGAATGACCATCAGGAAGGACAACTCCAAGAGCCAAG
      T Y N S A L K S R M T I R K D N S K S Q
301  TTTTCTTAATAATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGTGCCAGAC
      V F L I M N S L Q T D D S A M Y Y C A R
361  ATGGAACTTACTACGGAATGACTACGACGGGGATGCTTGGACTACTGGGGTCAAGGAA
      H G T Y Y G M T T G D A L D Y W G Q G
421  CCTCAGTCACCGTCTCCTCAG^GTAAGAATGCCCTAGA
      T S V T V S S

```

B. M200 V_L sequences
[NA, SEQ ID NO: 21; AA, SEQ ID NO: 22]

```

1   ACGCGTCCACCATGGATTTCAGGTGCAGATTTCAGCTTCCGTAATCAGTGCCTCAG
      M D F Q V Q I F S F L L I S A S
61   TCATAATGTCCAGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTC
      V I M S R G Q I V L T Q S P A I M S A S
121  TAGGGGAACGGGTCACCATGACCTGCACTGCCAGTTCAAGTGTCAGTCCAATTACTTG
      L G E R V T M T C T A S S S V S S N Y L
181  ACTGGTACCAGCAGAAGCCAGGATCCGCCCCAATCTCTGGATTATAGCACATCCAACC
      H W Y Q Q K P G S A P N L W I Y S T S N
241  TGGCTTCTGGAGTCCCAGCTCGTTCAGTGGCAGTGGCTGGGACCTCTTACTCTCTCA
      L A S G V P A R F S G S G S G T S Y S L
301  CAATCAGCAGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCTCGTT
      T I S S M E A E D A A T Y Y C H Q Y L R
361  CCCCACCGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAAC^GTAAGTAGAATCCAAAGT
      S P P T F G G G T K L E I K
421  CTAGA

```

FIGURE 5

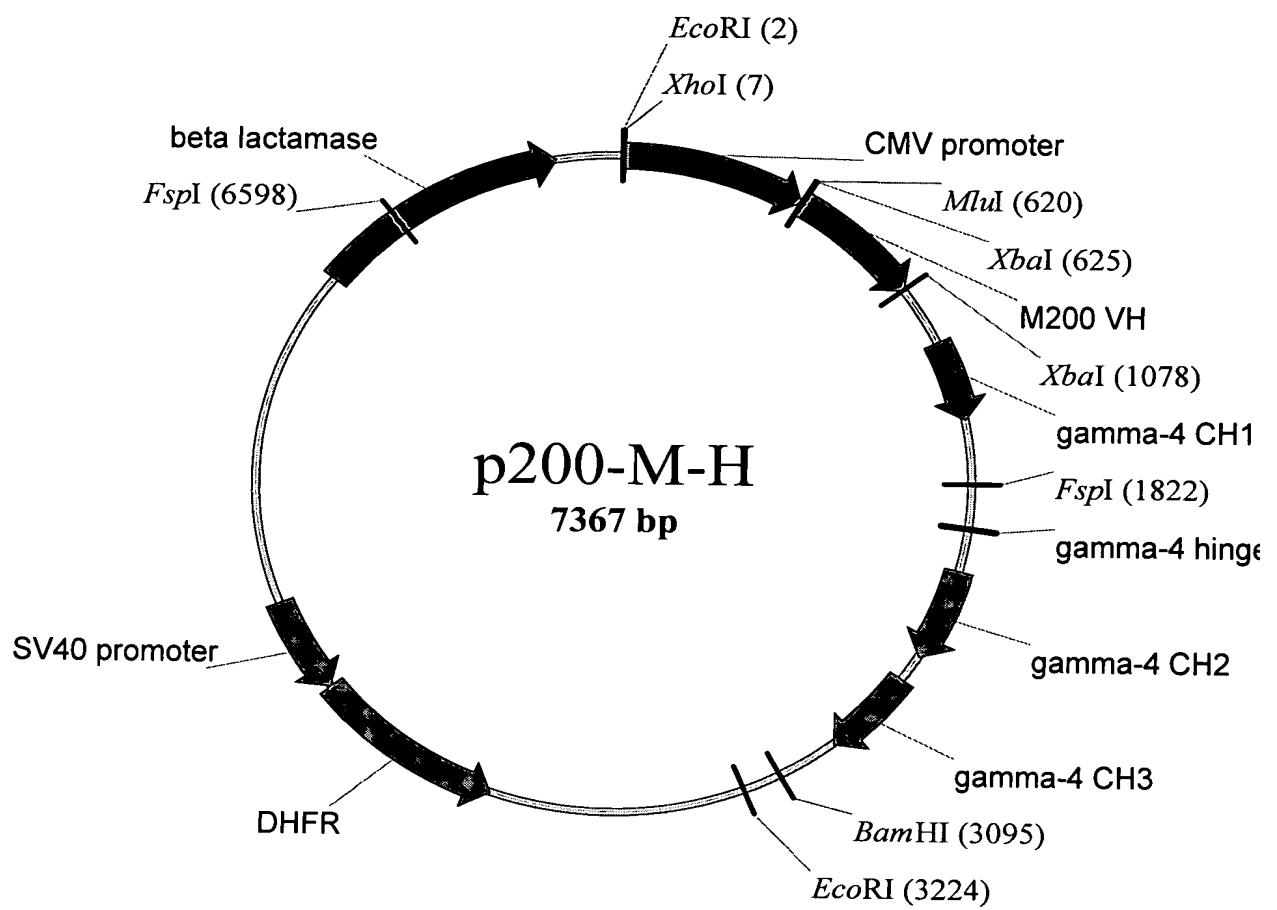


FIGURE 6

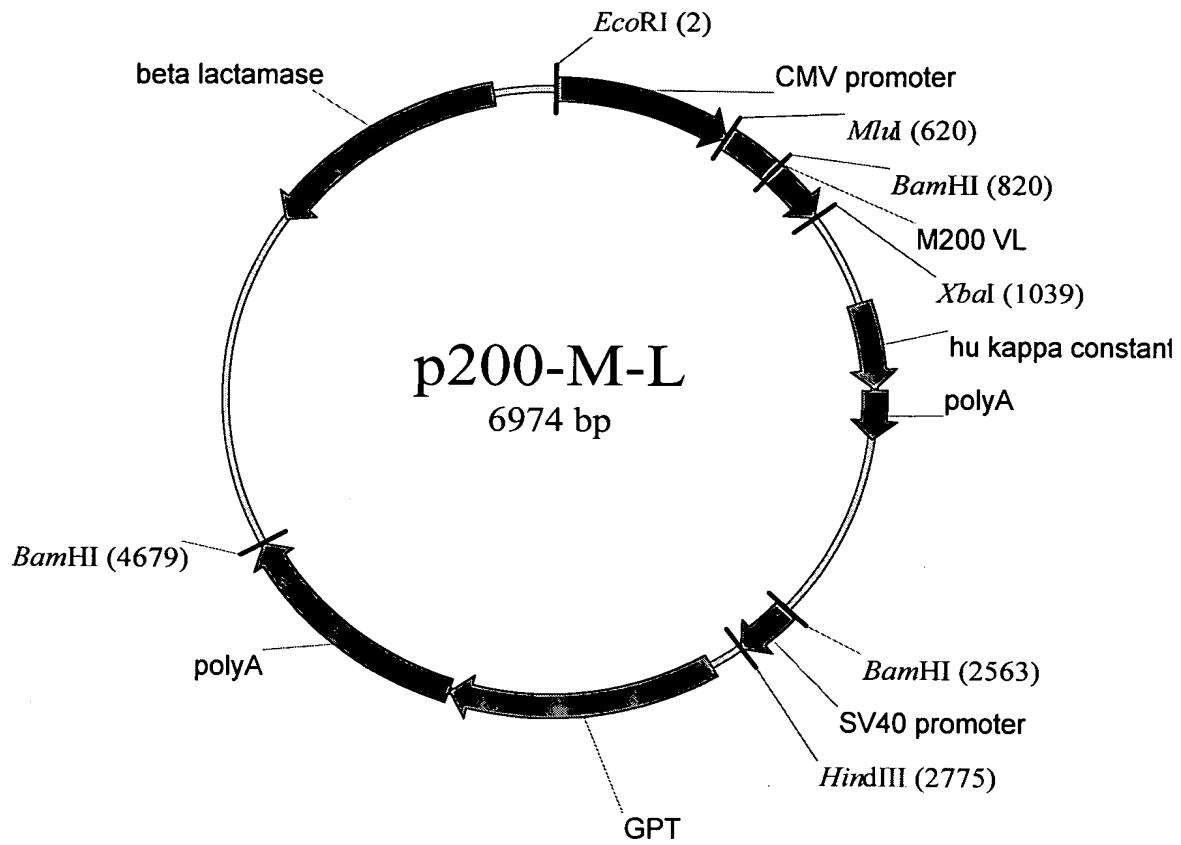


FIGURE 7

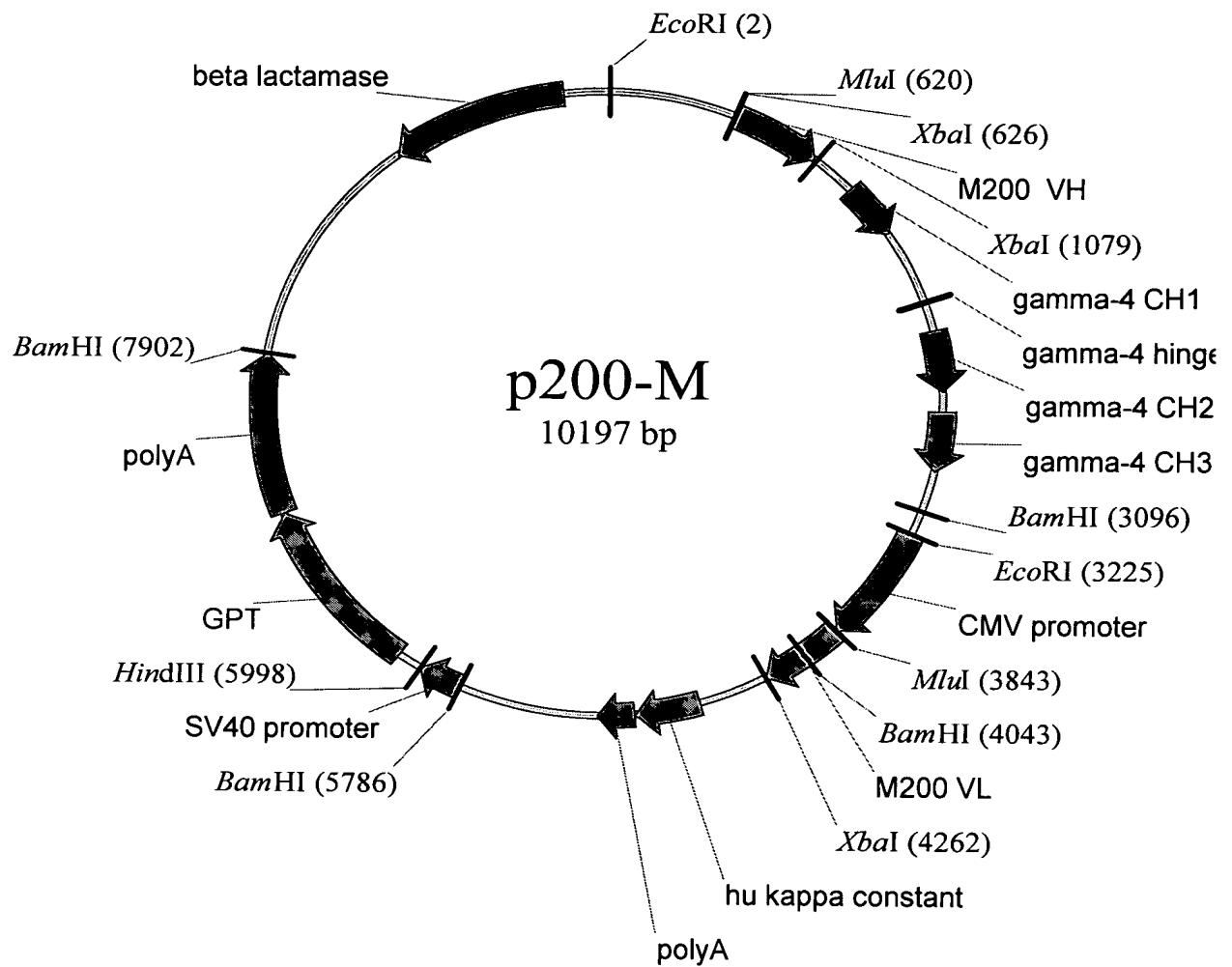


FIGURE 8

**M200 COMPLETE HEAVY CHAIN DNA SEQUENCE
(SEQ ID NO: 23)**

CAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGGGCCCTCACAGGCCGTCC
ATCACATGCACCCTCAAGGTTCTCATTAACCGACTATGGTGTCACTGGGTTCGC
CAGCCTCCAGAAAGGGTCTGGAGTGGCTGGTAGTGATTGGAGTGATGGAAGCTCA
ACCTATAATTAGCTCTCAAATCCAGAACATGACCACAGGAAGGACAACCTCAAGAGC
CAAGTTTCTTAATAATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGT
GCCAGACATGGAACTTACTACCGAATGACTACGACGGGGATGCTTGGACTACTGG
GGTCAAGGAACCTCAGTCACCGTCTCCTCAGCTTCCACCAAGGGCCATCCGTCTC
CCCCTGGGCCCTGCTCCAGGAGCACCTCCAGAGAGCACAGCCGCCCTGGGCTGCC
GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGGAACTCAGGCGCCCTGACC
AGCGCGTGACACCTTCCCAGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTACCGTGCCCTCCAGCAGCTTGGGACGAAGACCTACACCTGCAACGTA
GATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTCAAATATGGTCCC
CCATGCCCATATGCCAGCACCTGAGTTCTGGGGGACCATCAGTCTCCTGTT
CCCCAAAACCAAGGACACTCTCATGATCTCCGGACCCCTGAGGTACGTGCGTG
GTGGTGGACGTGAGCCAGGAAGACCCGAGGTCCAGTTCAACTGGTACGTGGATGGC
GTGGAGGTGCTAATGCCAAGACAAAGCCGGGGAGGAGCAGTTCAACAGCACGTAC
CGTGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAACGGCAAGGAGTAC
AAGTGCAAGGTCTCCAACAAAGGCCCTCCGCTCCATCGAGAAAACCATCTCCAAA
GCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCATCCCAGGAGGAG
ATGACCAAGAACCAAGGTGAGCCCTGACCTGCTGGTCAAAGGCTTCTACCCAGCGAC
ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAACTACAAGACCAAGC
CCCGTGTGGACTCCGACGGCTCCTCTACAGCAGGCTAACCGTGGACAAG
AGCAGGTGGCAGGAGGGAAATGTCTCTCATGCTCCGTGATGCATGAGGCTCTGCAC
AACCACACACAGAACAGGCCCTCCCTGTCTGGTAAA

**M200 COMPLETE LIGHT CHAIN DNA SEQUENCE
(SEQ ID NO: 24)**

CAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCATCTCTAGGGGAACGGGTC
ACCATGACCTGCACTGCCAGTTCAAGTGTAAAGTCCAATTACTTGCACGGTACCA
CAGAACGCCAGGATCCGCCCTCAATCTCTGGATTATAGCACATCCAACCTGGCTTCT
GGAGTCCCAGCTCGTTCAAGTGGCAGTGGCTGGGACCTCTTACTCTCACAATC
AGCAGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAAGTATCTCGTTCC
CCACCGACGTTGGTGGAGGCACCAAGCTGGAAATCAAACGAACGTGGCTGCACCA
TCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGAACTGCCTCTGTT
GTGTGCCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAGGTGGAT
AACGCCCTCCAATCGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC
AGCACCTACAGCCTCAGCAGCACCCGTACGCTGAGCAAAGCAGACTACGAGAACAC
AAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TTCAACAGGGAGAGTGT

FIGURE 9

M200 COMPLETE HEAVY CHAIN AMINO ACID SEQUENCE
(SEQ ID NO: 25)

QVQLKESGPLVAPSQSLISITCTISGFSLTDYGVHWVRQPPGKGLEWLVVIWSDGSS
TYNSALKSRMTIRKDNSKSQVFLIMNSLQTDDSAMYYCARHGTYGYGMTTGDALDYW
GQGTSVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT
SGVHTFPAPVLQSSGLYSLSSVVTVPSSSLGTKTTCNVVDHKPSNTKVDKRVESKYGP
PCPSCPAPEFLGGPSVFLFPPPKDKTLMSRTPEVTCVVVDVSQEDPEVQFNWYVDG
VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIETISK
AKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

M200 COMPLETE LIGHT CHAIN AMINO ACID SEQUENCE
(SEQ ID NO: 26)

QIVLTQSPAAMSASLGERTMTCASSSVSSNYLHWYQQKPGSAPNLWIYSTSNLASGVP
ARFSGSGSGTYSLTISSMEAEDAATYYCHQYLRSPPTFGGGTKLEIKRTVAAPSVFIFP
PSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSTL
TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 10

F200 COMPLETE HEAVY CHAIN DNA SEQUENCE
(SEQ ID NO: 27)

CAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCC
ATCACATGCACCATCTCAGGGTTCTCATTAACCGACTATGGTGTCACTGGGTTCGC
CAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGTAGTGATTGGAGTGATGGAAGCTCA
ACCTATAATTAGCTCTCAAATCCAGAACATGACCACATCAGGAAGGACAACCTCAAGAGC
CAAGTTTCTTAATAATGAACAGTCTCCAAACTGATGACTCAGCCATGTACTACTGT
GCCAGACATGGAACTTACTACCGAATGACTACGACGGGGATGCTTGGACTACTGG
GGTCAAGGAACCTCAGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTC
CCCCTGGCGCCCTGCTCCAGGAGCACCTCGAGAGCACAGCCGCCCTGGGCTGCCTG
GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGCGTGAACTCAGGCGCCCTGACC
AGCGCGTGACACCTCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTGGGACGAAGACCTACACCTGCAACGTA
GATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTCAAATATGGTCCC
CCATGCCCATCA

F200 COMPLETE HEAVY CHAIN AMINO ACID SEQUENCE
(SEQ ID NO: 28)

QVQLKESGPGLVAPSQSLSI TCTISGFSLTDYGVHWVRQPPGKGLEWLVVIWSDGSS
TYNSALKSRMTIRKD NSKSQVFLIMNSLQTDDSAMYYCARHGTYYGM TTGDALDYW
GQGTSVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALT
SGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGP
PCPS

FIGURE 11

huM200 COMPLETE HEAVY CHAIN DNA SEQUENCE
(SEQ ID NO: 29)

GAGGTGCAGCTGGTGGAGTCAGGAGGAGGCCTGGTGCAGCCCCGAGGAAGCCTGAGA
CTGTCATGCCCGCCTCAGGGTTCTCATTAACCGACTATGGTGTCACTGGGTTCCG
CAGGCCCGAGGAAGGGTCTGGAGTGGCTGGTGGTATTGGAGTGATGGAAGCTCA
ACCTATAATTCACTCAAATCCAGAACGACCATCTCAAAGGACAACGCCAAGAAC
ACCGTGTACTTACAGATGAACAGTCTCAGAGCTGAGGACACCGCCGTGTACTACTGT
GCCAGACATGGAACTTACTACCGAATGACTACGACGGGGATGCTTGGACTACTGG
GGTCAAGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCATCCGTCTC
CCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTG
GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGAACTCAGGCGCCCTGACC
AGCGCGTGACACCTCCCGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTGGGACGAAGACCTACACCTGCAACGTA
GATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTCAAATATGGTCCC
CCATGCCCATCATGCCAGCACCTGAGTTCTGGGGGACCATCAGTCTCCTGTT
CCCCAAAACCCAAGGACACTCTCATGATCTCCGGACCCCTGAGGTACAGTGC
GTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGATGGC
GTGGAGGTGATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTAACAGCACGTAC
CGTGTGGTCAGCGTCCTCACCGTCTGCACCAGGACTGGCTGAACGGCAAGGAGTAC
AAGTGAAGGTCTCAAACAAAGGCCTCCGCTCCATCGAGAAAACCCTCCAAA
GCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCCTGCCCCCATCCCAGGAGGAG
ATGACCAAGAACCAAGGTGACGCTGACCTGCCTGGTCAAAGGCTTACCCAGCGAC
ATCGCCGTGGAGTGGAGAGCAATGGGAGCCGGAGAACAACTACAAGACCAACGCCT
CCCGTGCTGGACTCCGACGGCTCCTCTACAGCAGGCTAACCGTGGACAAG
AGCAGGTGGCAGGAGGGGAATGTCTTCTATGCTCCGTGATGCATGAGGCTCTGCAC
AACCAACTACACACAGAACAGCCTCTCCCTGTCTGGTAAA

huM200 COMPLETE LIGHT CHAIN DNA SEQUENCE
(SEQ ID NO: 30)

GAAATTGTTCTCACCCAGTCTCCAGCAACCCCTCTCTCTCTCCGGGGAACGGGCT
ACCCCTCCTGCACTGCCAGTTCAAGTGTCACTTCAATTACTGCACGGTACCAAG
CAGAACGCCAGGACAGGGCCCCCGTCTCCTCATTATAGCACATCCAACCTGGCTTCT
GGAGTCCCAGCTCGTTCAAGTGGCAGTGGGTCTGGGACCTCTTACACCCCTACAATC
AGCAGCCTCGAGCCAGAACGATTTCGCCGTCTATTACTGCCACCGAGTATCTCGTT
CCACCGACGTTGGTGGAGGCACCAAGGTCGAATCAAACGAACGGTACGGCTGCACCA
TCTGTCTTCACTTCCGCCATCTGATGAGCAGTTGAAATCTGGAACACTGCCTCTGTT
GTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGAT
AACGCCCTCCAATCGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC
AGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAACAC
AAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TTCAACAGGGAGAGTGT

FIGURE 12

huM200 COMPLETE HEAVY CHAIN AMINO ACID SEQUENCE
(SEQ ID NO: 31)

EVQLVESGGGLVQPGGSLRLSCAASGFLTDYGVHWVRQAPGKGLEWLVVIWSDGSS
TYNSALKSRMTISKDNAKNTVYLQMNSLRAEDTAVYYCARHGTYYGMTTGDALDYW
GQGTLTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVWNSGALT
SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTTCNVVDHKPSNTKVDKRVESKYGP
PCPSCPAPEFLGGPSVFLFPPPKPKDTLMISRTPETCVVVDSQEDPEVQFNWYVDG
VEVHNNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK
AKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLGK

huM200 COMPLETE LIGHT CHAIN AMINO ACID SEQUENCE
(SEQ ID NO: 32)

EIVLTQSPATLSLSPGERATLSCTASSSVSSNYLHWYQQKPGQAPRLLIYSTSNLASGVP
ARFSGSGSGTSYTLTISSLEPEDFAVYYCHQYLRSPPTFGGGTKVEIKRTVAAPSVFIFP
PSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSTL
TLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

FIGURE 13

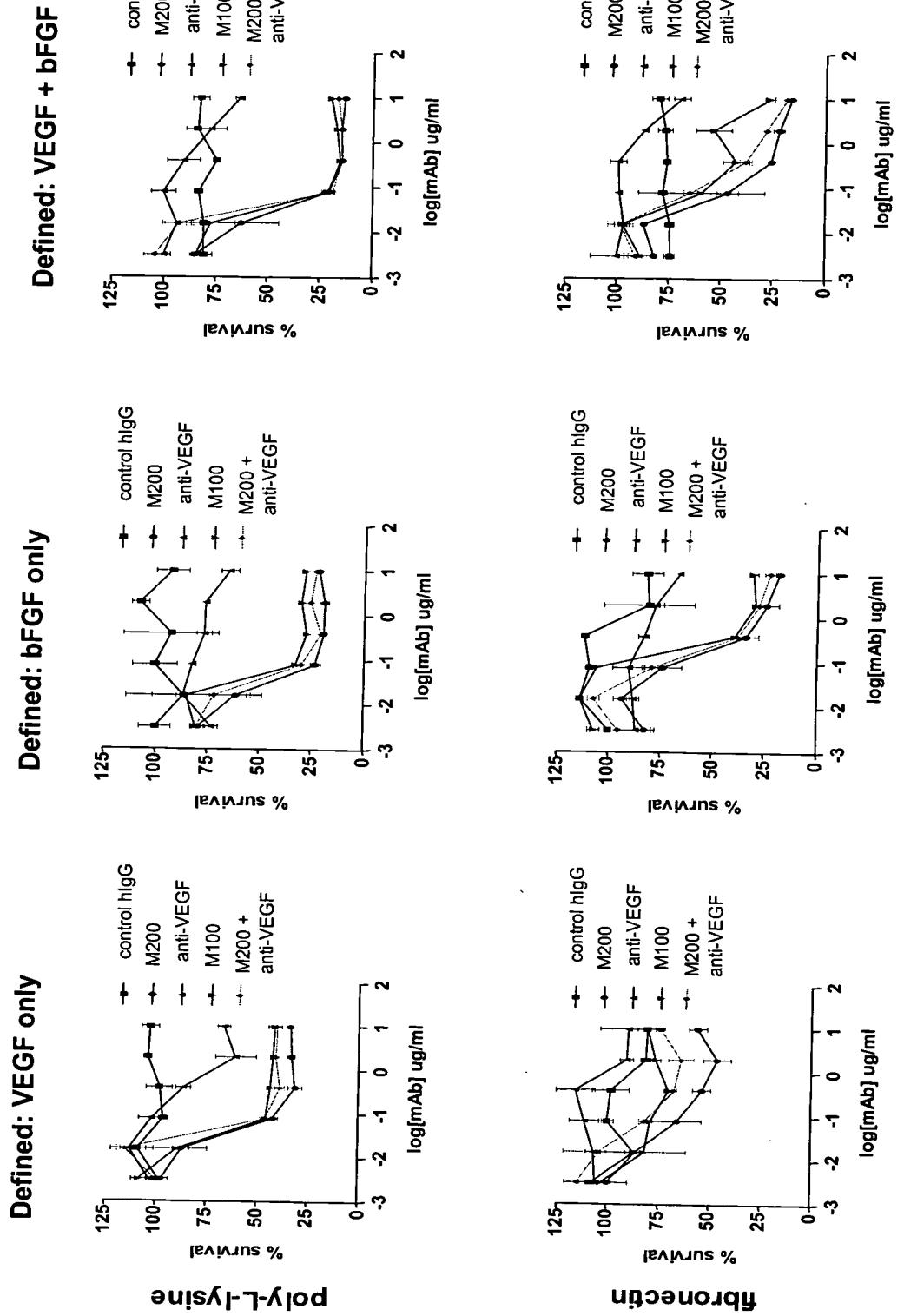
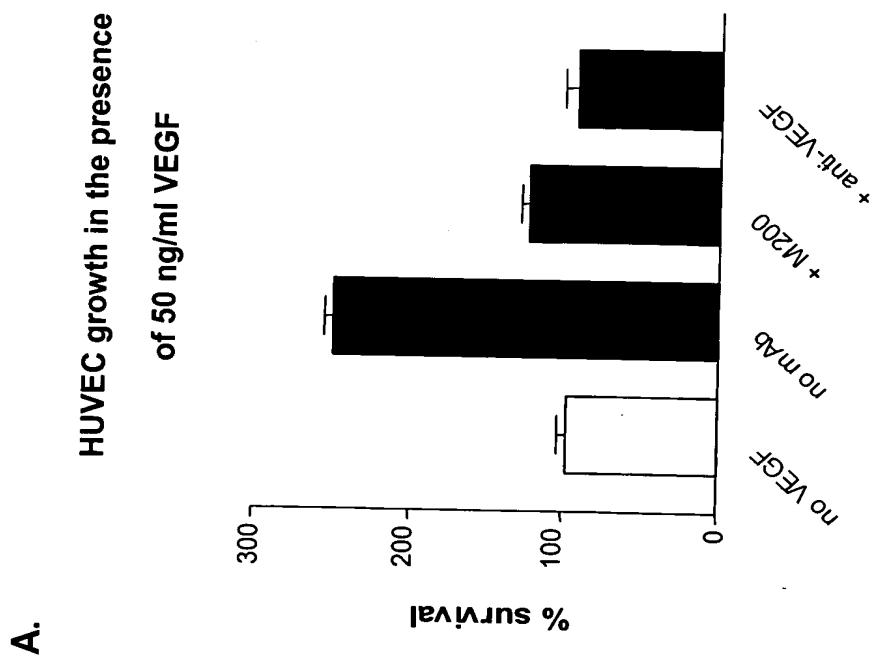


FIGURE 14



B.

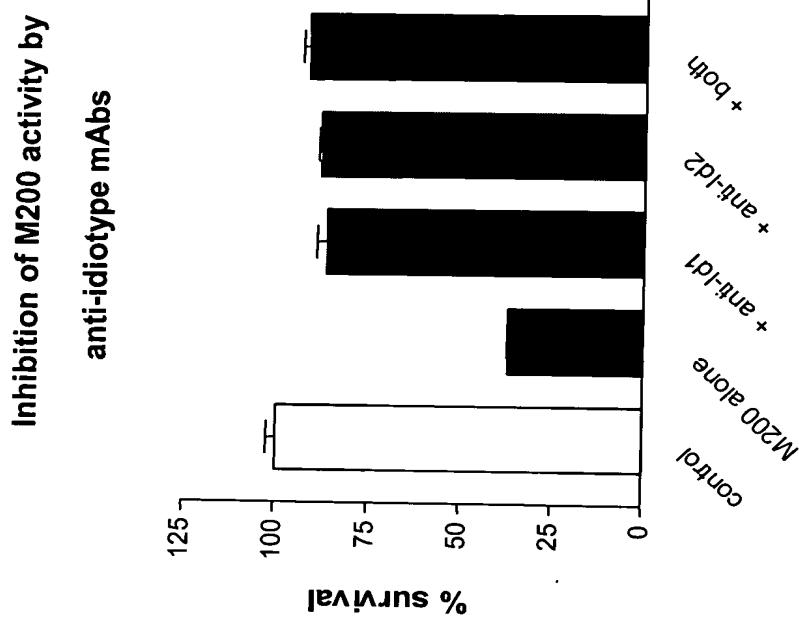
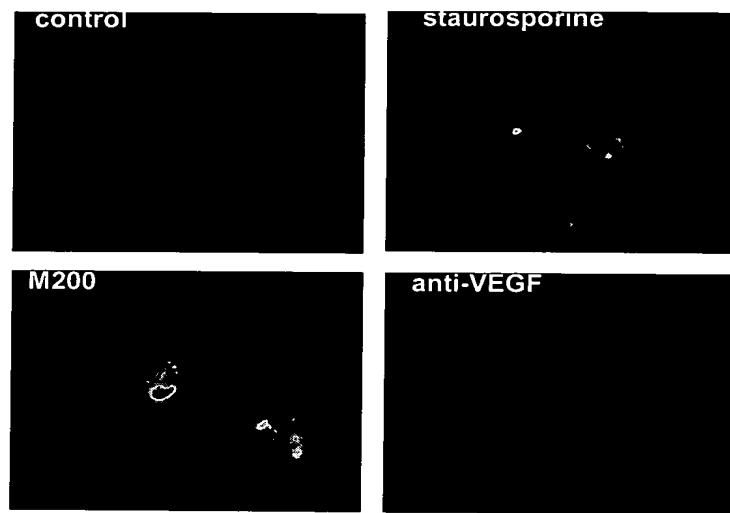


FIGURE 15

A.

**Visualization of Annexin V positive
cells by Immunofluorescence**



B.

**Quantification of Annexin V positive
cells by flow cytometry**

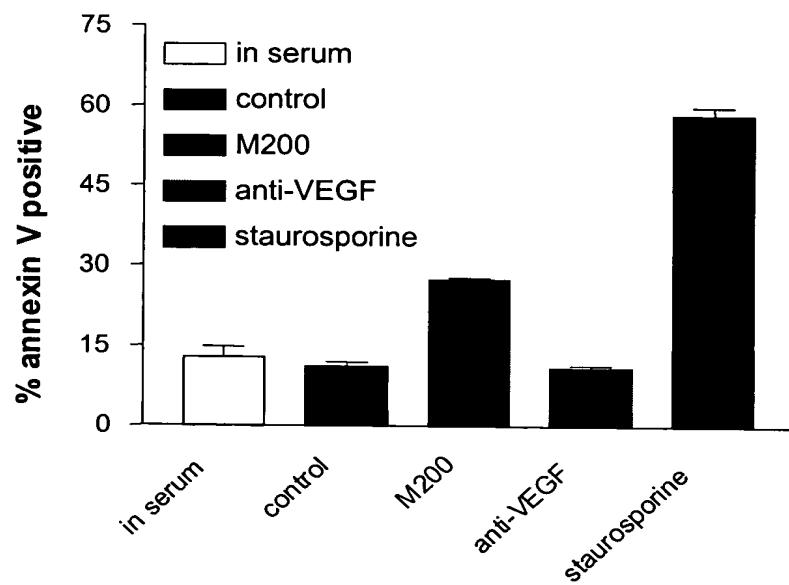
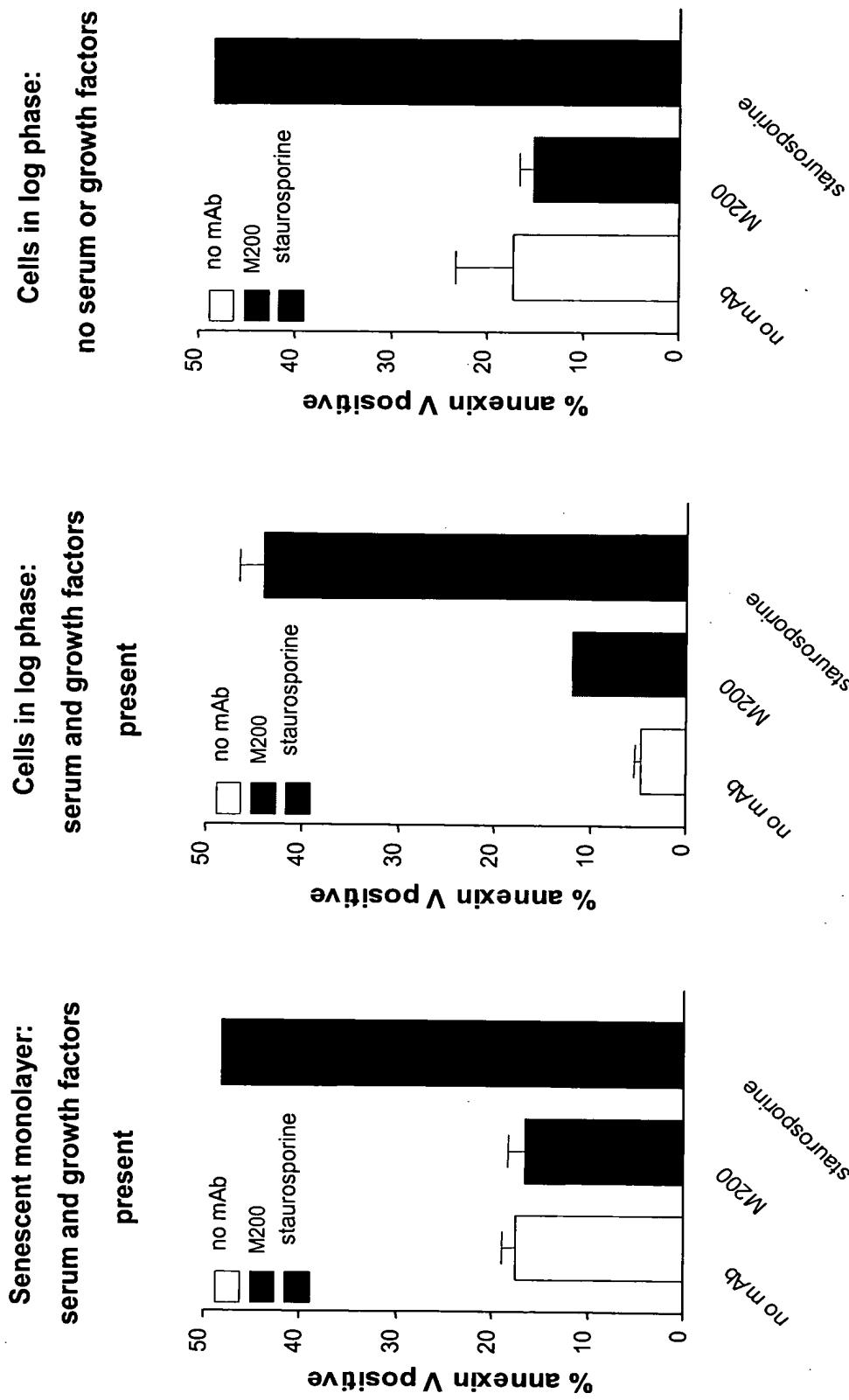


FIGURE 16

FIGURE 17



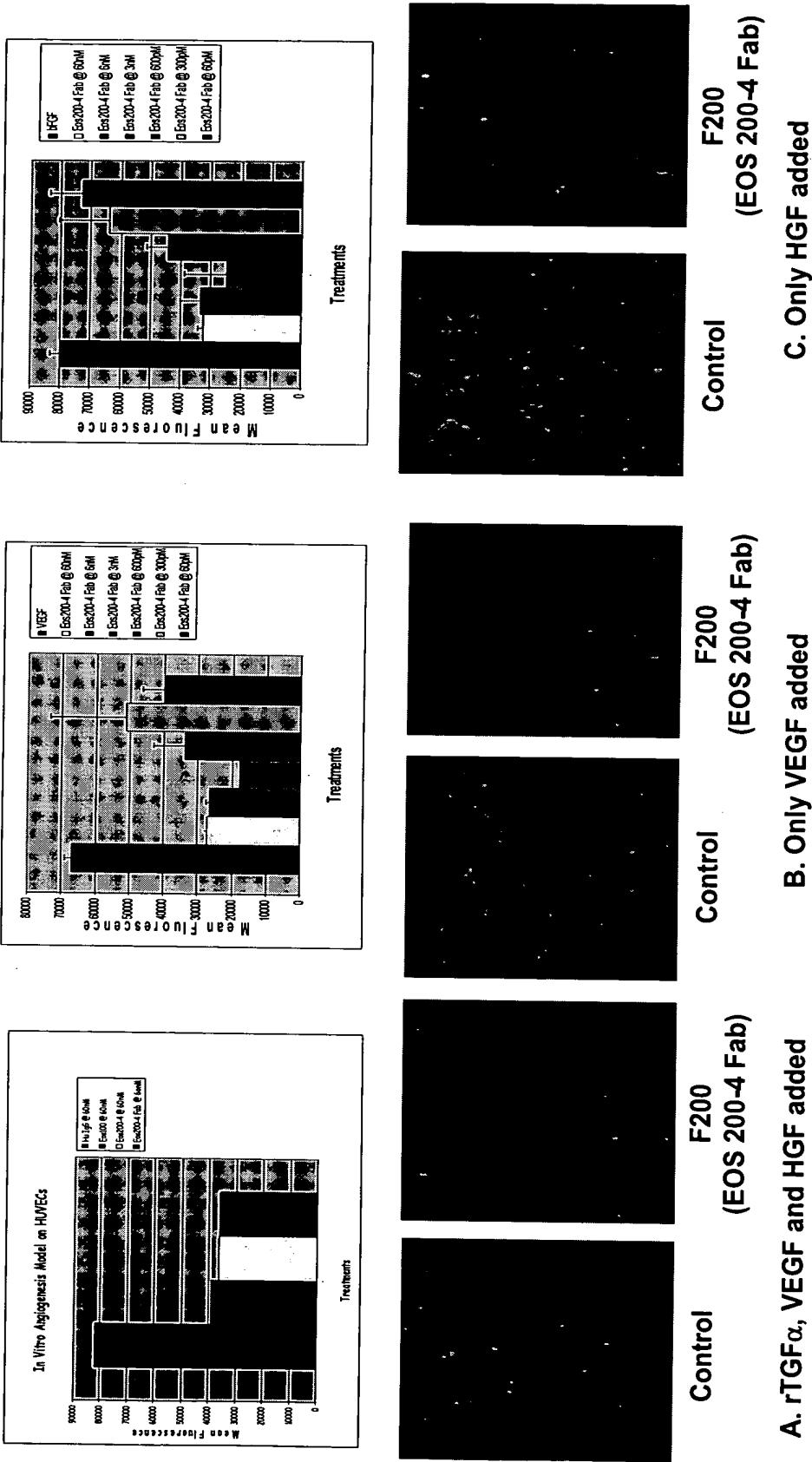


FIGURE 19

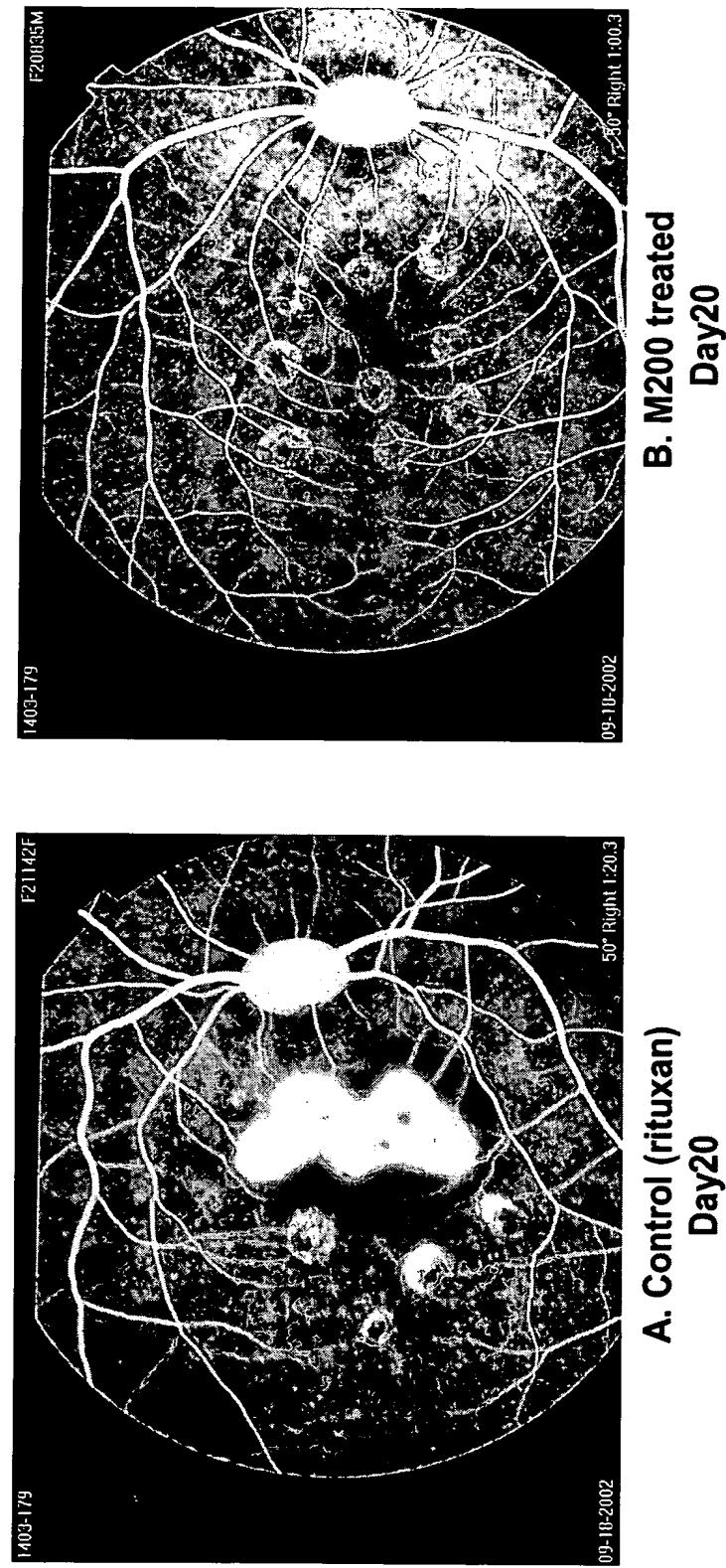


FIGURE 20

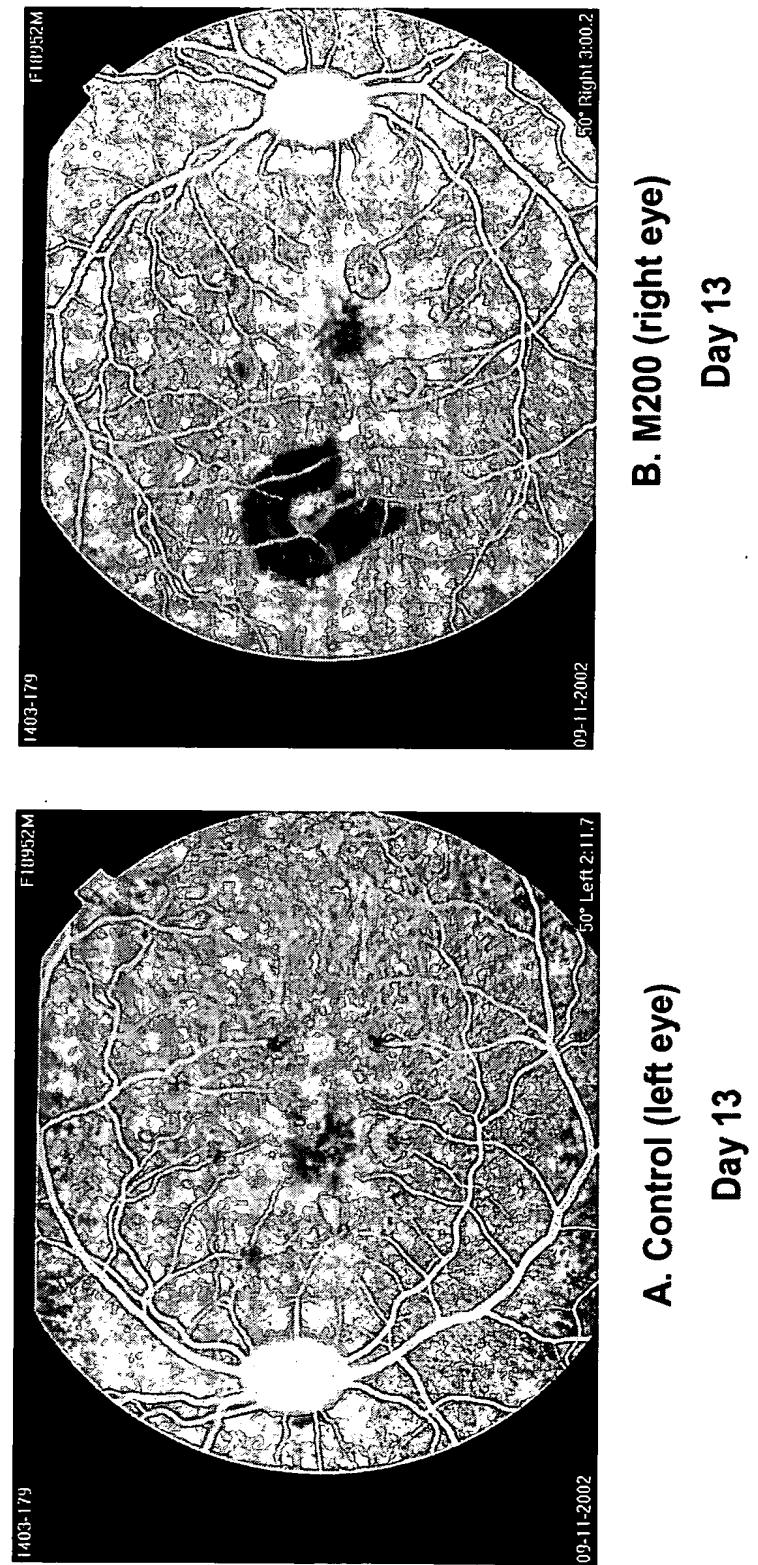


FIGURE 21

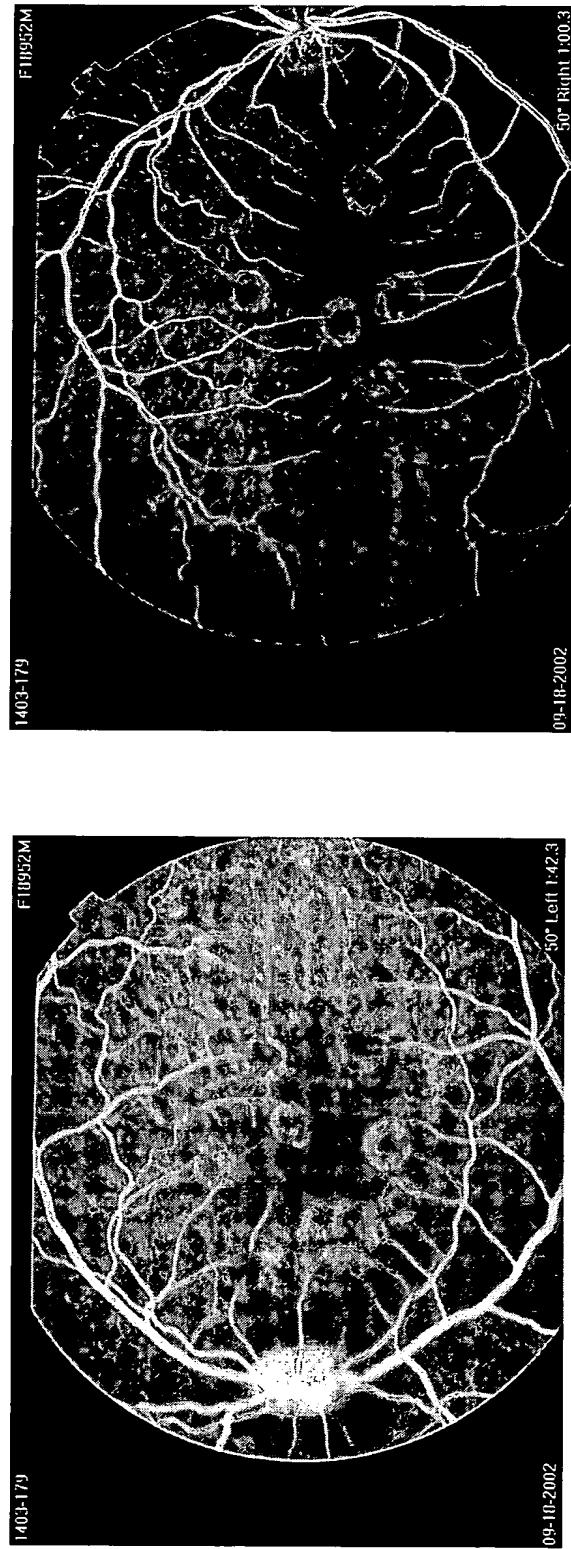


FIGURE 22

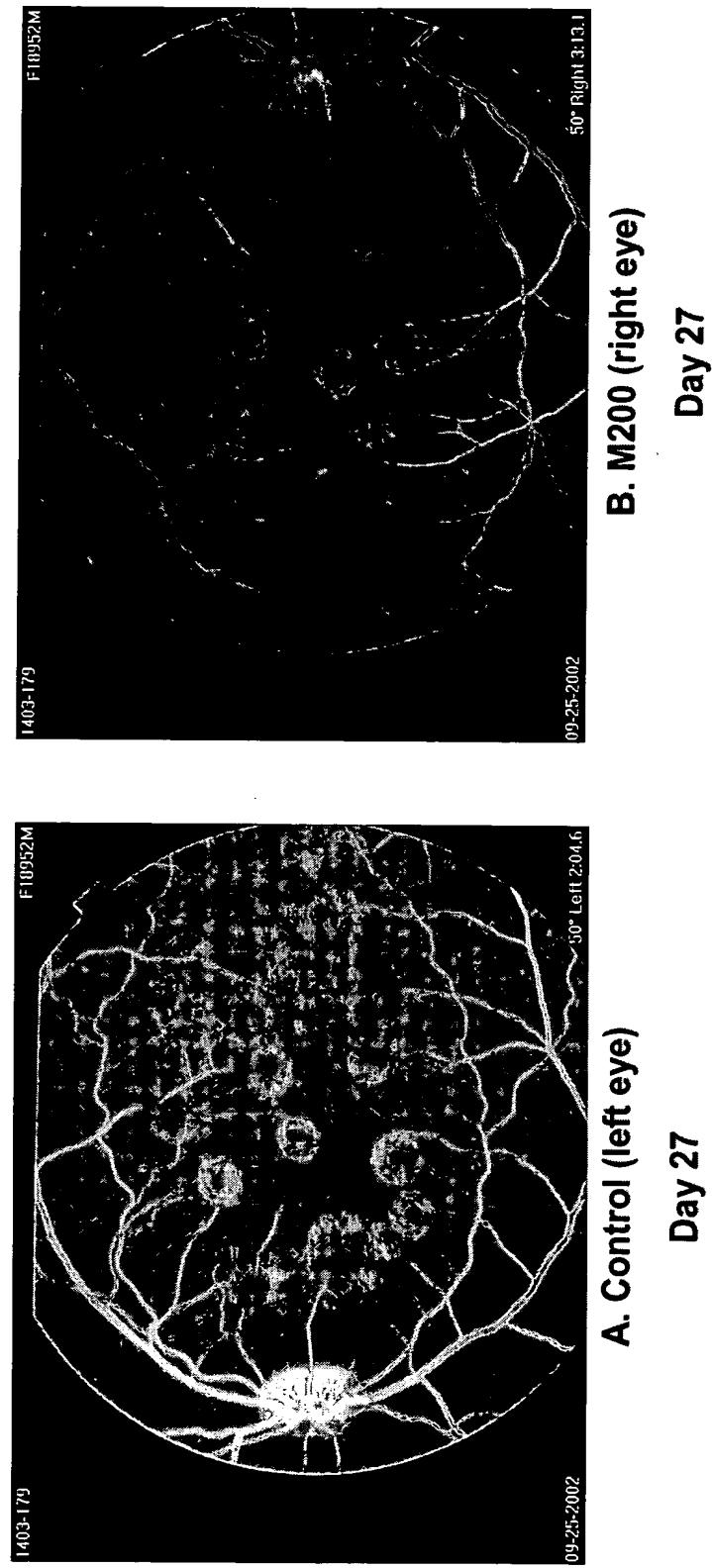


FIGURE 23

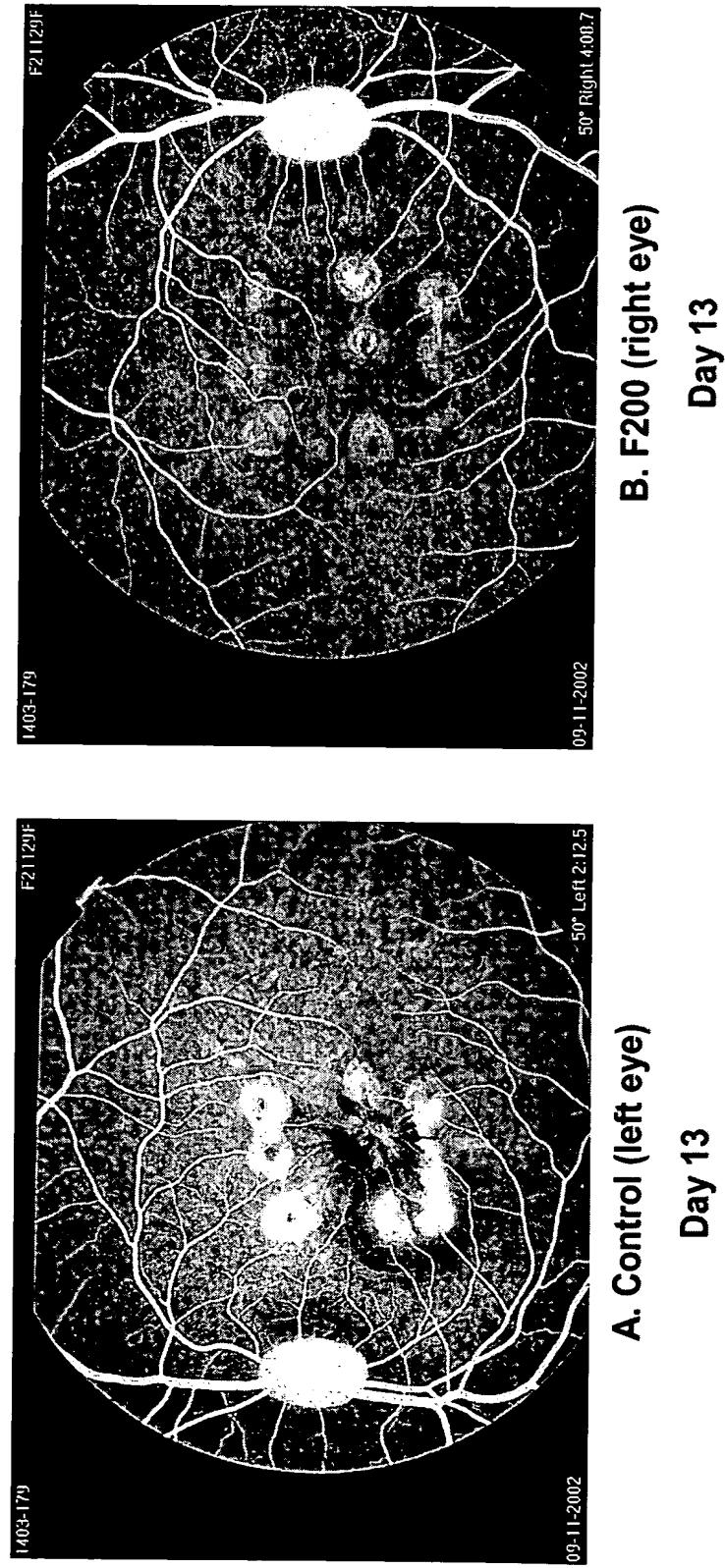


FIGURE 24

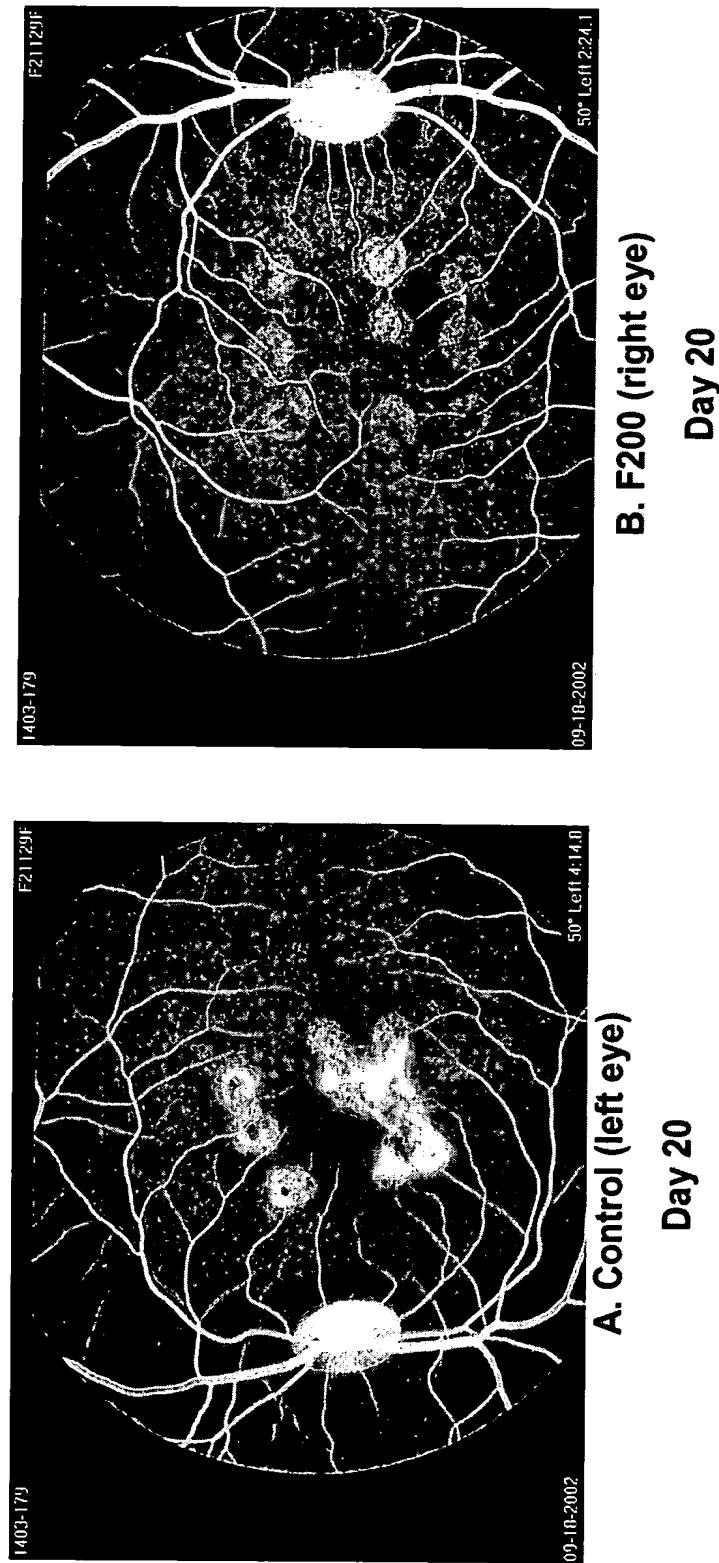
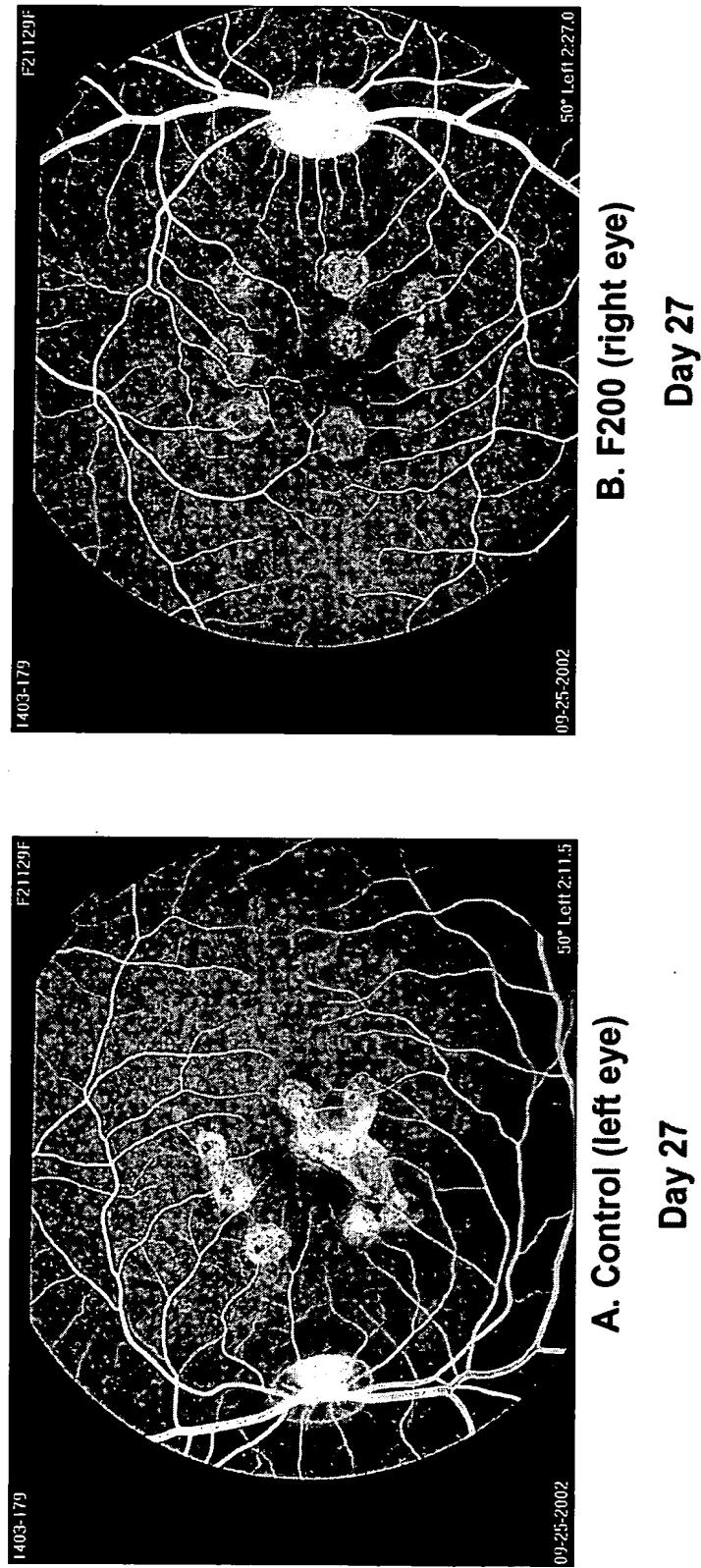


FIGURE 25



Competition ELISA 112103

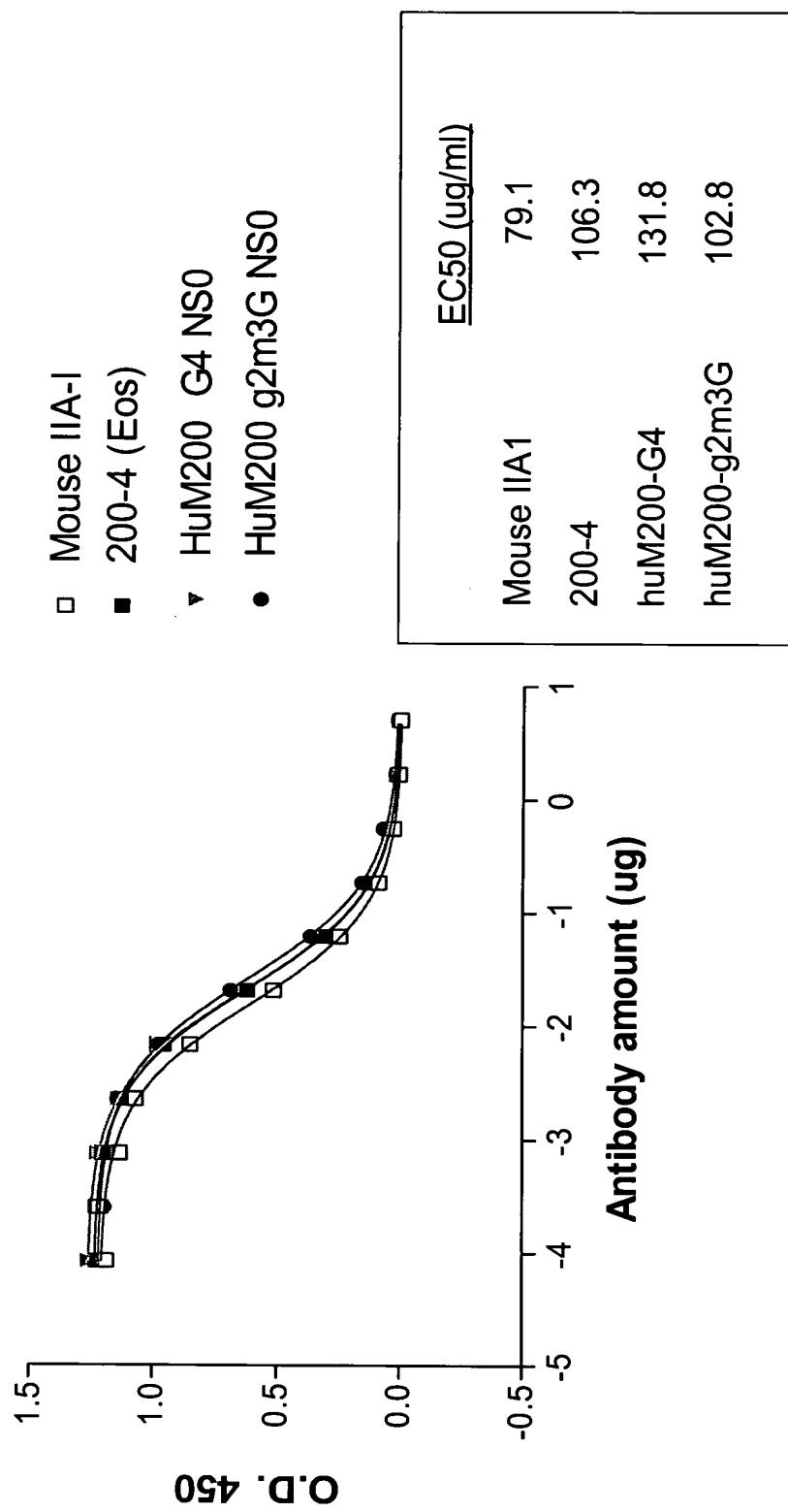


FIGURE 26